

LENGTH: 1920

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: No

US-08-746-789A-1

Alignment Scores:

Pred. No.:	5.85e-51	Length:	1920
Score:	445.00	Matches:	84
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-08-978-217-7 (1-84) x US-08-746-789A-1 (1-1920)

QY 1 AsnCysAlaLeuGluGluLeuAgleuvalPheGlyProLeuGlyAspGlnLeuHisAla 20

Db 424 AATGTGTCCTGGAGGAGCTGCCTGCGCTGCTGGCCCTGGGGACCACTCATGCC 483

QY 21 GluLeuAgaPleuThrSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40

Db 484 CACCTGCGGAGACCTCACTTCCAGCTCTTGATGAGCTGAGTGGATCATGGCTGC 543

QY 41 GluLysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProheAspGlnLyser 60

Db 544 GAGGAGGATGGATGGCTCCAGGAGGCCCTAACACCCAGGAGCAG 603

QY 61 ProheAlaGlnGluLeuAspAspGlyGlnDinalaserProTyRHisProGlySer 80

Db 604 CCCTTGGCCAGGAGCTGTCAGCAGGAGCCCTAACACCCGGAGC 663

QY 81 CysGlyAlaGly 84

Db 664 TGTGGCGGAGGA 675

RESULT 2

US-09-04-879A-139/C

; Sequence 139, Application US/09404879A

; PATENT NO. 6468546

; GENERAL INFORMATION:

; APPLICANT: King, Gordon E.

; APPLICANT: Algate, Paul A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.462C2

; CURRENT APPLICATION NUMBER: US/09/404, 879A

; CURRENT FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 393

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 92

; LENGTH: 551

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-404-879A-92

Alignment Scores:

Pred. No.:	0.497	Length:	551
Score:	72.00	Matches:	31
Percent Similarity:	39.81%	Conservative:	10
Best Local Similarity:	30.10%	Mismatches:	32
Query Match:	16.18%	Indels:	31
DB:	4	Gaps:	5

SEQ ID NO: 139

LENGTH: 521

TYPE: DNA

ORGANISM: Homo sapien

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: (1)..(521)

OTHER INFORMATION: n = A,T,C or G

US-09-404-879A-139

Alignment Scores:

Pred. No.:	0.461	Length:	521
Score:	72.00	Matches:	31
Percent Similarity:	39.81%	Conservative:	10
Best Local Similarity:	30.10%	Mismatches:	32
Query Match:	16.18%	Indels:	31
DB:	4	Gaps:	5

US-08-978-217-7 (1-84) x US-09-404-879A-92 (1-551)

QY 6 GluLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22

Db 354 GAGTTCATCTTCTTCATCTTCTAGGCCGCTTTCATAACTCTACCTCTCTC 295

QY 23 ArgPheLeuThrSerSerSerSerSerSerSerSerSerSerSerSerSerSer 42

Db 294 ACTCATCACGAGCTTTCAGC-----TTCTTCAGCTTGGAGGG 250

QY 43 AspGlyMetAla-----PheGlnGluAlaLeuAspProGly--- 54

Db 249 AGTGGCCAGGGCCTCTGAGCACGGCCAGCTCTTCBACAGCTGGATCTACGGTT 190

QY 55 -----ProheAspGlnLyserProheAspGlnLyserProheAspGlnLyser 67

Db 189 CAAGAGGCCACCTCTAGCCCTAGCCCTGCGCCGCGCCGCTTCCTTCTCCT-CACATTCTC 131

QY 68 AspAspGlyGlnGlnAlaserProTyRHis-----ProGlySer 80

Db 130 GCTGGAGGCCGCTCACTCGCTCTGATCATCTGCCCTGCTGCTGAGAACGCTGATCT 71

QY 81 Cysglyala 83
 |||:::
 Db 70 TGGCTCA 62

RESULT 4

US-09-404-879A-107/C
 Sequence 107, Application US/09404879A
 Patent No. 6468546
 GENERAL INFORMATION:
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: King, Gordon E.
 APPLICANT: Algate, Paul A.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.462C2
 CURRENT APPLICATION NUMBER: US/09/404,879A
 CURRENT FILING DATE: 1999-09-24
 NUMBER OF SEQ ID NOS: 393
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 107
 LENGTH: 555
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-404-879A-107

Alignment Scores:
 Pred. No.: 0.502 Length: 555
 Score: 72.00 Matches: 31
 Percent Similarity: 39.81% Conservative: 10
 Best Local Similarity: 30.10% Mismatches: 32
 Query Match: 16.18% Indels: 31
 DB: 4 Gaps: 5

US-08-978-217-7 (1-84) × US-09-404-879A-107 (1-555)

QY 6 GluLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGluLeu 22
 |||:::
 Db 358 GAGTTCACATCTTCTCATCTTTAACGCCCGTTTCATAACCTTCATACCTCTC 299

QY 23 ArgAspLeuThrSerSerSerSerAspGluLeuSerTripleLeuGluLeuGluLys 42
 |||:::
 Db 298 ACTCTCATCAGCAGCTTTTCAGC-----TTCTCAGCTTTCAGGC 254

QY 43 AspGlyMetAla-----PheGlnGluAlaLeuAspProGly-- 54
 |||:::
 Db 253 AGTGGCCAGGCCCTCTGAGCACGCCAGCTCTCAACCAAGCTGGATCCTACGGT 194

QY 55 -----ProHeAspGlyGlySerProHeAlaGlnLeu 67
 |||:::
 Db 193 CAAGGAGGCCACCTCAGCTCAGCTTGTTCCGGCCGCTTCCT-CAACTTC 135

QY 68 AspAspGlyGlyGlnAlaSerProTyRis-----ProGlySer 80
 |||:::
 Db 134 GCTGGAGGCCGCTCAGCTCAGCTCTGCTGCTGAGAACTGGATCT 75

QY 81 Cysglyala 83
 |||:::
 Db 74 TGGCTCA 66

RESULT 5

US-08-306-691B-23/C
 Sequence 23, Application US/08306691B
 Patent No. 573039
 GENERAL INFORMATION:
 APPLICANT: Calabretta, Bruno
 APPLICANT: Skorski, Tomasz
 TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
 NUMBER OF SEQUENCES: 55
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
 STREET: Two Penn Center, Suite 1800

CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19102

COMPUTER READABLE FORM:
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/305,691B
 FILING DATE: September 15, 1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 REFERENCE/DOCKET NUMBER: 8321-8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-8303
 TELEFAX: (215) 574-0396
 TELEX: No. 574039E

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2301 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

US-08-306-691B-23

Alignment Scores:
 Pred. No.: 3.39 Length: 2301
 Score: 72.00 Matches: 31
 Percent Similarity: 39.81% Conservative: 10
 Best Local Similarity: 30.10% Mismatches: 32
 Query Match: 16.18% Indels: 31
 DB: 1 Gaps: 5

US-08-978-217-7 (1-84) × US-08-306-691B-23 (1-2301)

QY 6 GluLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGluLeu 22
 |||:::
 Db 553 GAGTTCACATCTTCTCATCTTTAACGCCGGTTTCATAACCTTCATACCTCTC 494

QY 23 ArgAspLeuThrSerSerSerSerAspGluLeuSerTripleLeuGluLeuGluLys 42
 |||:::
 Db 493 ACTCTCATCAGCAGCTTTTCAGC-----TTCTCAGCTTTCAGGGC 449

QY 43 AspGlyMetAla-----PheGlnGluAlaLeuAspProGly-- 54
 |||:::
 Db 448 AGTGGCCAGGCCCTCTGAGCACGGTCAGCTCTCAACCAAGCTGGATCCTACGGT 389

QY 55 -----ProHeAspGlyGlySerProHeAlaGlnLeu 67
 |||:::
 Db 388 CAAGGAGGCCACCTCAGCTCAGCTGTTCCGGCCGCTTCCT-CAACTTC 330

QY 68 AspAspGlyGlyGlnAlaSerProTyRis-----ProGlySer 80
 |||:::
 Db 329 GCTGGAGGCCGCTCAGCTCAGCTCTGCTGCTGCTGAGAACTGGATCT 270

QY 81 Cysglyala 83
 |||:::
 Db 269 TGGCTCA 261

RESULT 6

PCR-US93-06251-78/C
 Sequence 78, Application PC/RUS9306251
 GENERAL INFORMATION:
 APPLICANT: Wickstrom, Eric and Rife, Jason P.
 TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing Stereospecific Alkylphosphonates and Arylphosphonates

Db 25220 GATGCCCTCACCT-----GGCTGTGGCAACCGGA 2546
 RESULT 8
 US-09-351-215-1
 ; Sequence 1, Application US/09351215
 ; Patent No. 6087488
 ; GENERAL INFORMATION:
 ; APPLICANT: Ganetzky, Barry S.
 ; APPLICANT: Titus, Steven A.
 ; TITLE OF INVENTION: Polynucleotides Encoding Herg-3
 ; FILE REFERENCE: 960296.94550
 ; CURRENT APPLICATION NUMBER: US/09/351,215
 ; CURRENT FILING DATE: 1999-07-12
 ; EARLIER APPLICATION NUMBER: 08/956,242
 ; EARLIER FILING DATE: 1997-10-22
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 LENGTH: 3141
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (248)..(2128)
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)
 OTHER INFORMATION: Unidentified at time of filing
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (3)
 OTHER INFORMATION: Unidentified at time of filing
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (12)
 OTHER INFORMATION: Unidentified at time of filing
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1568)..(1872)
 OTHER INFORMATION: Unidentified at time of filing
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (3126)
 OTHER INFORMATION: Unidentified at time of filing
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (3134)
 OTHER INFORMATION: Unidentified at time of filing
 US-09-351-215-1
 Alignment Scores:
 Pred. No.: 10.4
 Score: 66.50
 Percent Similarity: 36.84%
 Best Local Similarity: 27.37%
 Query Match: 14.94%
 DB: 4
 Length: 1473
 Matches: 26
 Conservative: 9
 Mismatches: 31
 Delets: 29
 Gaps: 4
 US-08-978-217-7 (1-84) x US-09-318-914-7 (1-1473)
 QY 7 Leu|Arg|Leu|Val|Phe|Gly|Pro|Leu|Gly|Asp|Gln|Leu|-----
 Db 1117 CTTGGGGCTCTTGGATATCAGGCCAGCCACCCCTCCCTAGCTACCGCTCT 1176
 QY 23 -----Arg|Asp|Leu|Thr|Ser|Ser|Ser|Ser|Asp|Glu|Leu|Ser|Trp|Ile|Leu|Leu| 40
 Db 1177 ACCCATCGCTCCACACTGAGCAGCAGCTCTAGACCTCGACCTCGATGTC----- 1224
 QY 41 Glu|Lys|Asp|Gly|Met|Ala|Phe|Gln|Glu|Ala|-----Asp|Pro|Gly|Pro|He 56
 Db 1225 -----TCTGGCAGAGCGCCAGAGCTGGTCTGGTCTGGAGTGAAGTGAGTGGCTGC-----
 QY 57 Asp|-----Gln|Gly|Ser|Pro|He|Ala| 63
 Db 1279 GACACAGAACACAGCTGGTGGGAGCTGCCAGCAGCAGTGGCAATCTCTCTGC 1338
 QY 64 Glu|Glu|Leu|Leu|Asp|Asp|Gly|Gln|Glu|Leu|Ser|Pro|Gly|Asp|Gly|Leu|Leu| 78
 Db 1339 AGTCATGACCTGGAGAGTGGAGAAGTCAGGTCTCCAGGCC 1383
 RESULT 10
 US-08-935-711-1/c
 ; Sequence 1, Application US/080555713
 ; Patent No. 595508
 ; GENERAL INFORMATION:
 ; APPLICANT: SATHE, GANESH
 ; APPLICANT: MOONEY, JEFFREY
 ; APPLICANT: BERGMA, DERK
 ; APPLICANT: HALSEY, WENDY

TITLE OF INVENTION: CDNA CLONE HE04D54 THAT ENCODES A HUMAN 7-TRANS NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: RITTER & PRESTIA
 ADDRESSEE: RITTER & PRESTIA
 STREET: P.O. BOX 980 TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING STATE: PA. CITY: VALLEY FORGE
 COUNTRY: USA TITLE OF INVENTION: PROTEINS ZIP: 19482 COMPUTER READABLE FORM: MEDIUM TYPE: Discrete
 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/355,713
 FILING DATE: 23-OCT-1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/050,124
 FILING DATE: 18-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F.
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-70087
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEX: 846169
 FAX: 610-407-0701
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1594 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-955-713-1

Alignment Scores:
 Pred. No.: 13.5 Length: 1594
 Score: 60.00 Matches: 27
 Percent Similarity: 36.96% Conservative: 7
 Best Local Similarity: 29.35% Mismatches: 35
 Query Match: 14.83% Indels: 22
 DB: Gaps: 4

US-08-978-217-7 (1-84) x US-08-955-713-1 (1-1594)

Qy 12 GlyProLeuGlyAspGlnLeuHisAlaGlnLeuArg-----AspLeu 25
 Db 1114 GGCCCTCTGGCGCCTGCCTGCCAGACCACTGGCTTCGGATGGTGACCCCATGCT 1055

Qy 26 ThrSerSerSerSerSerAspGluLeuSerTripleLeuGluLeuGluLysAsp----- 43
 Db 1054 CACATAGCAAGAGGAGTGGCAGACTCCAGGGTACACTCCCTG 995

Qy 44 -----GlyMetAlaPheGlnGluAlaLeuAspProGlyProPro 56
 Db 994 GTGCCAGGGAGGCCAGGGCTGTGCCCCACCTGTAGCTGAGGCGAGGGCC 935

Qy 57 AspGlnLyserProHeaGlnGluLeu-----AspAspGlyGlnGln 72
 Db 934 GGAGAAGGT-----GCTCAGGAGCAGTGCCCTGTAGGAGCAGGATGCCACCA 884

Qy 73 AlaSerProThrProGlySerCysGlyAlaGly 84
 Db 883 GAGTCCCCGGCAACGGGGAGTGGCCACGGGA 848

RESULT 11 US-08-131-365B-37
 ; Sequence 37, Application US/08131365B
 ; Patent No. 5527690
 ; GENERAL INFORMATION:

APPLICANT: Brown, Michael S.
 APPLICANT: Briggs, Michael R.
 APPLICANT: Wang, Xiaodong
 APPLICANT: Goldstein, Joseph L.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
 TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: U.S.A.
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/131,365B
 FILING DATE: 01-OCT-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Parker, David L.
 REGISTRATION NUMBER: 32,165
 REFERENCE/DOCKET NUMBER: UTSD:372/PAR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 FAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4154 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: 167..3607
 US-08-131-365B-37

Alignment Scores:
 Pred. No.: 49 Length: 4154
 Score: 66.00 Matches: 21
 Percent Similarity: 47.62% Conservative: 9
 Best Local Similarity: 33.33% Mismatches: 23
 Query Match: 14.83% Indels: 10
 DB: Gaps: 2

US-08-978-217-7 (1-84) x US-08-131-365B-37 (1-4154)

Qy 22 IeuaRgAspIeuthSerSerSerSerAspGluLeuSerTripleLeuGluLeuGlu 41
 Db 1355 CTGAAGGATCTGGTGTGGCCATGAGGAAACAGACAGTG--CTATGGAG 1411

Qy 42 LysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProProAspGlyGlySerPro 61
 Db 1412 GGCCTGAAGACTGAGCTGGAGACACACTGACCCACCCCTCGATGCTGGCTCACCT 1471

Qy 62 PheAlaGlnGluLeuLeuAspAspGlyGlyGlnAlaSerProThrProAspGlyGlySerPro 81
 Db 1472 TIC-----GAGCAGGCCCTGTCCTTGGAGCAG 1504

Qy 82 GlyAlaGly 84
 Db 1505 GGCAGTGGC 1513

RESULT 12 US-08-668-123-37
 ; Sequence 37, Application US/08668123
 ; Patent No. 5527690
 ; GENERAL INFORMATION:

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0., Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/162, 809
 FILING DATE:
 CLASIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31, 815
 REFERENCE/DOCKET NUMBER: P-LJ 9503
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3546 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 2..2920
 Alignment Scores:
 Pred. No.: 63.3 Length: 3546
 Score: 64.50 Matches: 22
 Percent Similarity: 43.42% Conservative: 11
 Best Local Similarity: 28.95% Mismatches: 38
 Query Match: 1 Indels: 6
 DB: Gaps: 1
 US-08-162-809-9 (1-3546)
 US-08-978-217-7 (1-84) x US-08-162-809-9 (1-3546)
 Alignment Scores:
 Pred. No.: 64.4 Length: 3591
 Score: 64.50 Matches: 22
 Percent Similarity: 43.42% Conservative: 11
 Best Local Similarity: 28.95% Mismatches: 38
 Query Match: 1 Indels: 6
 DB: Gaps: 1
 US-08-978-217-7 (1-84) x US-08-162-809-13 (1-3591)
 Qy 13 ProleuGlyAspGlnLeuIleAlaGlnLeuArgAspIleThrSerSerSerSerAspGlu 32
 Db 2170 CCTCTCAGAGTAGTCACTACGGTACCGAGACCTGG-CTGCCGCACATCTGGCAACA 2228
 Qy 33 LeuSerTrpIleLeuLeuLeuGluIleAspGlyMetAlaPheGlnGluAlaLeuAsp 52
 Db 2229 GCAACTTGTCGCAAGTGTGACTTCGGCTCTCCGGCTTTGGAGGATGATCCAG 2288
 Qy 53 -----ProGlyProPheAspGlyIleSerProPheAlaLagInGluLeu 67
 Db 2289 CGCACCCCCACCTACAGCTCCCTGGAGCAAAATCCCATCAGTGTCGACAGCTCG 2348
 Qy 68 AspAspGlyIleGlnAlaSerProTyRHisProGlySerCysGlyAla 83
 Db 2349 AGGCCATCGCTTACCGCAATTCACTCGGCCAGCGACGCTGGAGCT 2396
 RESULT 15
 US-08-162-809-13
 Sequence 13, Application US/08162809
 Patent No. 5457048
 GENERAL INFORMATION:
 APPLICANT: Pasquale, Elena B.
 APPLICANT: Saljadi, Fereydoun G.
 TITLE OF INVENTION: NOVEL EPH RELATED TYROSINE KINASES
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CAMPBELL AND FLORES
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States of America
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0., Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/162, 809
 FILING DATE:
 CLASIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31, 815
 REFERENCE/DOCKET NUMBER: P-LJ 9503
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3591 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 2..2965
 US-08-162-809-13
 Alignment Scores:
 Pred. No.: 64.4 Length: 3591
 Score: 64.50 Matches: 22
 Percent Similarity: 43.42% Conservative: 11
 Best Local Similarity: 28.95% Mismatches: 38
 Query Match: 1 Indels: 6
 DB: Gaps: 1
 US-08-978-217-7 (1-84) x US-08-162-809-13 (1-3591)
 Qy 13 ProleuGlyAspGlnLeuIleAlaGlnLeuArgAspIleThrSerSerSerSerAspGlu 32
 Db 2215 CCTCTCAGAGATGACTACGGTACCGAGACCTGG-CTGCCGCACATCTGGCAACA 2273
 Qy 33 LeuSerTrpIleLeuLeuLeuGluIleAspGlyMetAlaPheGlnGluAlaLeuAsp 52
 Db 2274 GCAACTTGTCGCAAGTGTGACTTCGGCTCTCCGGCTTTGGAGGATGATCCAG 2333
 Qy 53 -----ProGlyProPheAspGlyIleSerProPheAlaLagInGluLeu 67
 Db 2334 CGCACCCCCACCTACAGCTCCCTGGAGCAAAATCCCATCAGTGTCGACAGCTCG 2393
 Qy 68 AspAspGlyIleGlnAlaSerProTyRHisProGlySerCysGlyAla 83
 Db 2394 AGGCCATCGCTTACCGCAATTCACTCGGCCAGCGACGCTGGAGCT 2441
 Search completed: March 15, 2003, 23:33:00
 Job time : 36.7601 secs